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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/776,874A

DATE: 12/12/2001 05
TIME: 11:51:23

Input Set : A:\ES.txt
Output Set: N:\CRF3\12112001\I776874A.raw

ENTERED

3 <110> APPLICANT: Pecker, Iris
 4 Vlodavsky, Israel
 5 Feinstein, Elena
 7 <120> TITLE OF INVENTION: POLYNUCLEOTIDE ENCODING A POLYPEPTIDE HAVING HEPARANASE
 ACTIVITY AND
 8 EXPRESSION OF SAME IN GENETICALLY MODIFIED CELLS
 10 <130> FILE REFERENCE: 01/22603
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/776,874A
 C--> 12 <141> CURRENT FILING DATE: 2001-12-12
 12 <150> PRIOR APPLICATION NUMBER: US 08/922,170
 13 <151> PRIOR FILING DATE: 1997-09-02
 15 <150> PRIOR APPLICATION NUMBER: US 09/109,386
 16 <151> PRIOR FILING DATE: 1998-07-10
 18 <150> PRIOR APPLICATION NUMBER: PCT/US98/17954
 19 <151> PRIOR FILING DATE: 1998-08-31
 21 <160> NUMBER OF SEQ ID NOS: 47
 23 <170> SOFTWARE: PatentIn version 3.1
 25 <210> SEQ ID NO: 1
 26 <211> LENGTH: 27
 27 <212> TYPE: DNA
 28 <213> ORGANISM: Artificial sequence
 30 <220> FEATURE:
 31 <223> OTHER INFORMATION: synthetic oligonucleotide
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 34 ccatccta atcgactcact ataggc 27
 37 <210> SEQ ID NO: 2
 38 <211> LENGTH: 24
 39 <212> TYPE: DNA
 40 <213> ORGANISM: Artificial sequence
 42 <220> FEATURE:
 43 <223> OTHER INFORMATION: synthetic oligonucleotide
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 46 gtagtgatgc catgtaactg aatc
 49 <210> SEQ ID NO: 3
 50 <211> LENGTH: 23
 51 <212> TYPE: DNA
 52 <213> ORGANISM: Artificial sequence
 54 <220> FEATURE:
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 58 actcactata gggctcgagc ggc 23
 61 <210> SEQ ID NO: 4
 62 <211> LENGTH: 22
 63 <212> TYPE: DNA
 64 <213> ORGANISM: Artificial sequence
 66 <220> FEATURE:
 67 <223> OTHER INFORMATION: synthetic oligonucleotide
 69 <400> SEQUENCE: 4

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70 gcatcttagc cgtcttctt cg
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76 <213> ORGANISM: Artificial sequence
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87 <212> TYPE: DNA
88 <213> ORGANISM: Artificial sequence
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130 cgctgggtcc cctctccctt ggcgcctgc cccgacactgc gcaaggcacag gacgtcggtgg 240
132 acctggactt cttcacccag gagccgtgc acctgggtgag cccctcggtt ctgtccgtca 300
134 ccattgacgc caacctggcc acggacccgc ggttccat cctccctgggt tctccaaagc 360
136 ttctgtaccc ttgcagaggc ttgtctccctg cgtacactgag gtttggggc accaagacag 420
138 acttcctaatttttccatccca aagaaggaat caacctttga agagagaatg tactggcaat 480
140 ctcaagtc aa ccaggatatt tgcaaataatg gatccatccc tcctgtatgtg gaggagaatg 540
142 tacgggttggaa atggccctac caggagcaat tgctactccg agaacactac cagaaaaatg 600
144 tcaagaacag cacttactca agaagctctg tagatgtgct atacactttt gcaaactgct 660
146 caggactgga ctgtatctt ggcctaaatg cgttattaag aacagcagat ttgcagtggaa 720
148 acagttctaa tgctcagttg ctccctggact actgcttcc caaggggtat aacatttctt

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150	gggaactagg	caatgaacct	aacagttcc	ttaagaaggc	tgatatttc	atcaatgggt	780
152	cgcagtagg	agaagattat	attcaattgc	ataaaactct	aagaaaagtcc	accttcaaaa	840
154	atgcaaaact	ctatggct	gatgtggc	agcctcgaag	aaagacggct	aagatgctga	900
156	agagcttcc	gaaggctgg	ggagaagtg	ttgattcagt	tacatggcat	cactactatt	960
158	tgaatggac	gactgctacc	agggaaagatt	ttctaaaccc	tgatgtattg	gacattttta	1020
160	tttcatctgt	gcaaaaagtt	ttccagggtt	ttgagagcac	caggcctggc	aagaaggct	1080
162	gtttaggaga	aacaagctct	gcatatggag	gcggagcgcc	cttgctatcc	gacacccttg	1140
164	cagctggctt	tatgtggctg	gataaaatttg	gcctgtcage	ccgaatggga	atagaagtgg	1200
166	tgtgaggca	agtattctt	ggagcaggaa	actaccattt	agtggatgaa	aacttcgatc	1260
168	cttacactga	ttattggcta	tctcttctgt	tcaagaaattt	ggtgggcacc	aaggtgttaa	1320
170	tggcaagcgt	gcaaggttca	aagagaagga	agcttcgagt	ataccattcat	tgcacaaaaca	1380
172	ctgacaatcc	aaggataaaa	gaaggagatt	taactctgt	tgccataaac	ctccataacg	1440
174	tcaccaagta	cttgcggta	ccctatccctt	tttctaacaa	gcaagtggat	aaataccctc	1500
176	taagacctt	gggacctcat	ggattacttt	ccaaatctgt	ccaactcaat	ggtotaactc	1560
178	taaagatggt	ggatgatcaa	acttgccac	ctttaatgg	aaaacctctc	cggccaggaa	1620
180	gttcaactgg	cttgcagct	ttctcatata	gttttttgt	gataagaaat	gccaaagttg	1680
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188 <211> LENGTH: 543
189 <212> TYPE: PRT
190 <213> ORGANISM: Homo sapiens

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193 Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu Leu
194 1 5 10 15
195 Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg Pro
196 20 25 30
197 Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu Pro
198 35 40 45
199 Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala Asn
200 50 55 60
201 Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Leu Gly Ser Pro Lys Leu
202 65 70 75 80
203 Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly Gly
204 85 90 95
205 Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Glu Ser Thr Phe
206 100 105 110
207 Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys Lys
208 115 120 125
209 Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu Trp
210 130 135 140
211 Pro Tyr Gln Glu Gln Leu Leu Arg Glu His Tyr Gln Lys Lys Phe
212 145 150 155 160
213 Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr Thr Phe
214 165 170 175
215 Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu Leu
216 180 185 190
217 Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu Leu
218 195 200 205
219 Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly Asn
220

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247	210	215	220													
250	Glu	Pro	Asn	Ser	Phe	Leu	Lys	Lys	Ala	Asp	Ile	Phe	Ile	Asn	Gly	Ser
251	225															240
254	Gln	Leu	Gly	Glu	Asp	Tyr	Ile	Gln	Leu	His	Lys	Leu	Leu	Arg	Lys	Ser
255																255
258	Thr	Phe	Lys	Asn	Ala	Lys	Leu	Tyr	Gly	Pro	Asp	Val	Gly	Gln	Pro	Arg
259																270
262	Arg	Lys	Thr	Ala	Lys	Met	Leu	Lys	Ser	Phe	Leu	Lys	Ala	Gly	Gly	Glu
263																285
266	Val	Ile	Asp	Ser	Val	Thr	Trp	His	His	Tyr	Tyr	Leu	Asn	Gly	Arg	Thr
267																300
270	Ala	Thr	Arg	Glu	Asp	Phe	Leu	Asn	Pro	Asp	Val	Leu	Asp	Ile	Phe	Ile
271																320
274	Ser	Ser	Val	Gln	Lys	Val	Phe	Gln	Val	Val	Glu	Ser	Thr	Arg	Pro	Gly
275																335
278	Lys	Lys	Val	Trp	Leu	Gly	Glu	Thr	Ser	Ser	Ala	Tyr	Gly	Gly	Ala	
279																350
282	Pro	Leu	Leu	Ser	Asp	Thr	Phe	Ala	Ala	Gly	Phe	Met	Trp	Leu	Asp	Lys
283																365
286	Leu	Gly	Leu	Ser	Ala	Arg	Met	Gly	Ile	Glu	Val	Val	Met	Arg	Gln	Val
287																380
290	Phe	Phe	Gly	Ala	Gly	Asn	Tyr	His	Leu	Val	Asp	Glu	Asn	Phe	Asp	Pro
291																400
294	Leu	Pro	Asp	Tyr	Trp	Leu	Ser	Leu	Leu	Phe	Lys	Lys	Leu	Val	Gly	Thr
295																415
298	Lys	Val	Leu	Met	Ala	Ser	Val	Gln	Gly	Ser	Lys	Arg	Arg	Lys	Leu	Arg
299																430
302	Val	Tyr	Leu	His	Cys	Thr	Asn	Thr	Asp	Asn	Pro	Arg	Tyr	Lys	Glu	Gly
303																445
306	Asp	Leu	Thr	Leu	Tyr	Ala	Ile	Asn	Leu	His	Asn	Val	Thr	Lys	Tyr	Leu
307																460
310	Arg	Leu	Pro	Tyr	Pro	Phe	Ser	Asn	Lys	Gln	Val	Asp	Lys	Tyr	Leu	Leu
311																480
314	Arg	Pro	Leu	Gly	Pro	His	Gly	Leu	Leu	Ser	Lys	Ser	Val	Gln	Leu	Asn
315																495
318	Gly	Leu	Thr	Leu	Lys	Met	Val	Asp	Asp	Gln	Thr	Leu	Pro	Pro	Leu	Met
319																510
322	Glu	Lys	Pro	Leu	Arg	Pro	Gly	Ser	Ser	Leu	Gly	Leu	Pro	Ala	Phe	Ser
323																525
326	Tyr	Ser	Phe	Phe	Val	Ile	Arg	Asn	Ala	Lys	Val	Ala	Ala	Cys	Ile	
327																540
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331	<211>	LENGTH:	1721													
332	<212>	TYPE:	DNA													
333	<213>	ORGANISM:	Homo sapiens													
335	<220>	FEATURE:														
336	<221>	NAME/KEY:	CDS													
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338	<223>	OTHER INFORMATION:														

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345 Met Leu Leu Arg Ser Lys Pro Ala Leu Pro Pro Pro Leu Met Leu
346 1 5 10 15
348 ctg ctc ctg ggg ccg ctg ggt ccc ctc tcc cct ggc gcc ctg ccc cga 155
349 Leu Leu Leu Gly Pro Leu Gly Pro Leu Ser Pro Gly Ala Leu Pro Arg
350 20 25 30
352 cct gcg caa gca cag gac gtc gtg gac ctg gac ttc acc cag gag 203
353 Pro Ala Gln Ala Gln Asp Val Val Asp Leu Asp Phe Phe Thr Gln Glu
354 35 40 45
356 ccg ctg cac ctg gtg agc ccc tcg ttc ctg tcc gtc acc att gac gcc 251
357 Pro Leu His Leu Val Ser Pro Ser Phe Leu Ser Val Thr Ile Asp Ala
358 50 55 60
360 aac ctg gcc acg gac ccg cgg ttc ctc atc ctc ctg ggt tct cca aag 299
361 Asn Leu Ala Thr Asp Pro Arg Phe Leu Ile Leu Gly Ser Pro Lys
362 65 70 75
364 ctt cgt acc ttg gcc aga ggc ttg tct cct gcg tac ctg agg ttt ggt 347
365 Leu Arg Thr Leu Ala Arg Gly Leu Ser Pro Ala Tyr Leu Arg Phe Gly
366 80 85 90 95
368 ggc acc aag aca gac ttc cta att ttc gat ccc aag aag gaa tca acc 395
369 Gly Thr Lys Thr Asp Phe Leu Ile Phe Asp Pro Lys Lys Ser Thr
370 100 105 110
372 ttt gaa gag aga agt tac tgg caa tct caa gtc aac cag gat att tgc 443
373 Phe Glu Glu Arg Ser Tyr Trp Gln Ser Gln Val Asn Gln Asp Ile Cys
374 115 120 125
376 aaa tat gga tcc atc cct gat gtg gag gag aag tta cgg ttg gaa 491
377 Lys Tyr Gly Ser Ile Pro Pro Asp Val Glu Glu Lys Leu Arg Leu Glu
378 130 135 140
380 tgg ccc tac cag gag caa ttg cta ctc cga gaa cac tac cag aaa aag 539
381 Trp Pro Tyr Gln Glu Gln Leu Leu Arg Glu His Tyr Gln Lys Lys
382 145 150 155
384 ttc aag aac agc acc tac tca aga agc tct gta gat gtg cta tac act 587
385 Phe Lys Asn Ser Thr Tyr Ser Arg Ser Ser Val Asp Val Leu Tyr
386 160 165 170 175
388 ttt gca aac tgc tca gga ctg gac ttg atc ttt ggc cta aat gcg tta 635
389 Phe Ala Asn Cys Ser Gly Leu Asp Leu Ile Phe Gly Leu Asn Ala Leu
390 180 185 190
392 tta aga aca gca gat ttg cag tgg aac agt tct aat gct cag ttg ctc 683
393 Leu Arg Thr Ala Asp Leu Gln Trp Asn Ser Ser Asn Ala Gln Leu Leu
394 195 200 205
396 ctg gac tac tgc tct tcc aag ggg tat aac att tct tgg gaa cta ggc 731
397 Leu Asp Tyr Cys Ser Ser Lys Gly Tyr Asn Ile Ser Trp Glu Leu Gly
398 210 215 220
400 aat gaa cct aac agt ttc ctt aag aag gct gat att ttc atc aat ggg 779
401 Asn Glu Pro Asn Ser Phe Leu Lys Lys Ala Asp Ile Phe Ile Asn Gly
402 225 230 235
404 tcg cag tta gga gaa gat tat att caa ttg cat aaa ctt cta aga aag 827
405 Ser Gln Leu Gly Glu Asp Tyr Ile Gln Leu His Lys Leu Leu Arg Lys

Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa.



12/12/01

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/776,874A

DATE: 12/12/2001
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Input Set : A:\ES.txt
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L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:3199 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:47